```
        10              30              50
TCCTGCGTTATCCCCCTGATTCTGTGGATAACCGTATTNCCGCCTTTGAGTGAGCTGATA
        70              90             110
CCGCTCNCCNCAGCCGGAACGACCGAGCGCAGCGAGTCAGTGAGCGGAGGAAGCGGAAGAGC
       130             150             170
GCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACG
       190             210             230
ACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCA
       250             270             290
CTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTG
       310             330             350
TGAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCGAAA
       370             390             410
TTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCCACCGCGGTGGCGGCCGNCCGCTCTAGAA
       430             450             470
CTAGTGGATCCCCCGGNCTGCAGGGGGCACACACAGGCACACACATACACAGAATCCTCAGAT
       490             510             530
AACAGGAGGCAATAAATCCAACAGCACACGTTCAGAGAACAGTGTCCCTGCTGTCT
       550             570             590
TGCTAACAGCTGCCAATACCTCACTGAGTGCCTGCTCACACCAACATGGGCTCCAAGTGAGTT
       610             630             650
TCATTCGTCTGGGGCAGACTCCCTCCCCTCTTCCATAAAGGCTGCAGGAGACCTGTAGCTG
       670             690             710
TCACAGGACCTTCCCCTAAGAGCCCGGCAGGGGGAAGACTGCCCCAGTCGGCGGCCATCACCAT
                                          M
       730             750             770
GCTCCGGCCCATTCTGGATGCTCCCCAGCGGTTGCTGAAGGAGGGGAGAGCGGTCCCGGCA
 L   R   P   I   L   D   A   P   Q   R   L   L   K   E   G   R   A   S   R   Q
       790             810             830
```

FIG.1A

GCTGGTGCTGGTGGTGTATTCGTCGCTTTGCTCCTGGACAACATGTTGTTACTGTGGT
L L V V V F V A L L L D N M L F T V V
850   870   890

GGTGCCAATTGTGCCACCTTCCTATATGACATGGAGTTCAAAGAAGTCATCTCTTCTCT
V P I V P T F L Y D M E F K E V I S S L
910   930   950

GCACCTCGGGCATGCCGGAAGTTCCCACACATGCCCTCGCCTTTTCCACCAT
H L G H A G S S P H A L A S P A F S T L
970   990   1010

CTTCTCCTTCTTCAACAACAACACCGTGGCTGTTGAAGAAAAGCGTACCTAGTGGAATAGC
F S F F N N N T V A V E E S V P S G I A
1030   1050   1070

ATGGATGAATGACACTGCCAGCACCATCCCACCTCCAGCCACTGAAGCCATCTCAGCTCA
W M N D T A S T I P P A T E A I S A H
1090   1110   1130

TAAAAACAACTGCTTGCAAGGCACAGGTTTCTTGGAGGAAGAGACTACCCGGGTCGGGGT
K N C L Q G T G F L E E E T T R V G V
1150   1170   1190

TCTGTTTGCTTCAAAGGCTGTGATGCAACTTCTGGTCAACCCATTCGTGGGCCCTCTCAC
L F A S K A V M Q L L V N P F V G P L T
1210   1230   1250

CAACAGGATTGGATATCATATCCCCATGTTTGCTGGCTTTGTTATCATGTTTCTTCCAC
N R I G Y H I P M F A G F V I M F L S T
1270   1290   1310

AGTTATGTTTGCTTTTTCTGGGACCTATACTCTACTCTTTGTGGCCCGAACCCTTCAAGG
V M F A F S G T Y T L L F V A R T L Q G
1330   1350   1370

FIG.1B

```
CATTGGATCTTCATTTCATCTGTTGTTGCAGGTCTTGGAATGTGCTGGCCAGTGTCTACACTGA
 I  G  S  S  F  S  S  S  V  A  G  L  G  M  L  A  S  V  Y  T  D
              1390                            1410                1430

TGACCATGAGAGAGGAACGAGCCATGGGAACTGCTCTGGGGGGCCTGGCCTTGGGGTTGCT
 D  H  E  R  G  R  A  M  G  T  A  L  G  G  L  A  L  G  L  L
         1450                    1470                   1490

GGTGGGAGCTCCCTTTGGAAGTGTAATGTACGAGTTTGTTGGGAAGTCTGCACCCTTCCT
 V  G  A  P  F  G  S  V  M  Y  E  F  V  G  K  S  A  P  F  L
          1510                    1530                   1550

CATCCTGGCCTTCCTGCTGGATGGAGCACTCCAGCTTTGCATCCTCACAGCCTTC
 I  L  A  F  L  A  L  L  D  G  A  L  Q  L  C  I  L  Q  P  S
         1570                    1590                   1610

CAAAGTCTCTCTGAGAGTGCCAAGGGGACTCCCCTCTTTATGCTTCTCAAAGACCCTTA
 K  V  S  P  E  S  A  K  G  T  P  L  F  M  L  L  K  D  P  Y
          1630                    1650                   1670

CATCCTGGTGGCTGCAGGGTCCATCTGCTTTGCCAACATGGGGGTGGCCATCCTGGAGCC
 I  L  V  A  A  G  S  I  C  F  A  N  M  G  V  A  I  L  E  P
         1690                    1710                   1730

CACACTGCCCATCTGGATGATGCAGACCATGTGCTCCCCCAAGTGGCAGCTGGGTCTAGC
 T  L  P  I  W  M  M  Q  T  M  C  S  P  K  W  Q  L  G  L  A
         1750                    1770                   1790

TTTCTTGCCTGCCAGTGTGTCCTACCTAATCGGGACCAACCTCTTTGGTGTGTTGGCCAA
 F  L  P  A  S  V  S  Y  L  I  G  T  N  L  F  G  V  L  A  N
         1810                    1830                   1850

CAAGATGGGTCGGTGGCTGTGTTCCCTAATCGGGATGCTGGTAGTAGGTACCAGCTTGCT
 K  M  G  R  W  L  C  S  L  I  G  M  L  V  V  G  T  S  L  L
         1870                    1890                   1910

CTGTGTTCCTCTGGCTCACAAAAATTTGGTCTCATTGGCCCAATGCAGGGCTTGGCCT
```

FIG.1C

```
C  V  P  L  A  H  K  N  F  G  L  I  G  P  N  A  G  L  G  L
                              1950                    1970
TNCCATAGGCATGGTGGAATCTTCTATGATGCCCATCATGGGGCACCTGGTGGATCCACG
        1990                    2010                    2030
X  I  G  M  V  E  S  S  M  M  P  I  M  G  H  L  V  D  P  R
CCACACCTCGGGTGTATGGGAGTGTCCACGCCATCGCTGATGTGGCTTTTTGCATGGGCTT
H  T  S  V  Y  G  S  V  H  A  I  A  D  V  A  F  C  M  G  F
        2050                    2070                    2090
TGCTATAGGCTATTCTGAGTCAGGAGTGCCCCATGGAGACCCGGATGTATCAACCCAGAA
A  I  G  Y  S  E  S  G  L  P  H  G  O  P  D  V  S  T  Q  K
        2110                    2130                    2150
ACCTCTTCCCTGGACCAGTCACCATGGCTGACCCACGGCTCAGTGGCCTCAAAACCTCTG
P  L  P  W  T  S  H  H  G  *
        2170                    2190                    2210
CCTGGGATCTTTCTTCCTCCCCCTCCCATGGACACTGTCCCTGATACTCTTCTCACCTGTGT
        2230                    2250                    2270
AACTTGTAGCTCTTCMTCTATGCCTTGGTGCCGCAGTGGCCCATCTTTTATGGGAAGACA
        2290                    2310                    2330
GAGTGATGATGCACCYYCCCGCTGCTGTGAGGTTGATTAAACTTGAGCTGTGACGGGGTTCTG
        2350                    2370                    2390
CAAGGGGTGACTCATTGYATAGAGGTGGTAGTGAGTAATGTGCCCCTGAAACCAGTGGGG
        2410                    2430                    2450
TGACTGACAAGCCTCTTTAATCTGTTGCCTGATTTTCTCTGGCATAGCCCAACAGATCG
        2470                    2490                    2510
GAAGAGTGTTACCCTCTCTTTWCCCTCAAGCGTGTTCTTTCCCGGGTTTTCCCCAGCCGAGTT
```

FIG.1D

2530   2550   2570
GAGAAAATGTTCTCAGCATTGTCTTGCTGCCAAATGCCAGCKTGAAGAGTTWGGTATGKT
           2590   2610   2630
TTTCTNCCATTTATTTATTTATTWACTAAAGTGAATGATTTTACTGTGGYTAAAATCTA
           2650   2670   2690
GAGCTGCTAAAAGGGCTTTACCCTCAGTGAAAAGTGTCTTCTATTTNCATWATCTTTCAG
           2710   2730   2750
AAACWGGAGCCCATTTCTTCTTCTGGTGGAGTTATNGACATCCTCCTGACCNCCCCTGTGT
           2770   2790   2810
NTNCCTACCTNTACTGAACCTCTTAGACTCTNAGAAATAAAAGTAGAAGAAAGACAGAAA
           2830   2850   2870
AATTAACTGATTAGAGCCCAAGATTTCATGGAAGAAGTTAAAAGAAAACTGCCTTGGAAAT

CCCTC

FIG.1E

Homology Alignment between HATBG78 and
the Rat Amine Transporter

```
  1 MLRPILDAPQRLLKEGRASRQLVLVVVFVALLLDMMFTVVVPIVPTFLY   50
    ||..:|||||||||.||..|||||||||||||||:||||||||||||||
  1 MQVVTGAPQRLLKEGRQSRKLVLVVVFVALLLDNMLLTVVVPIVPTFLY   50

 51 DMEFKEVISSLHLGHAGSSPHALASPAFSTIFSFFNNNTVAVEESVPSGI  100
    |||. ||||.||. ...:|.||.|||||||||||||||:.|..||:.|| .
 51 ATEFKDSNSSLHRGPSVSSQQALTSPAFSTIFSFFONTTTTVEEHVPFRV  100

101 AWMNDTASTIPPPATEAISAHKNNCLQGTGFLEEETTRVGVLFASKAVMQ  150
    .| .:||||.|||.|||..|.:|||||||.:|.:|||||||||.:||:||
101 TW...TNGTIPPPVTEASSVPKNNCLQGIEFLEEENVRIGILFASKALMQ  147

151 LLVNPFVGPLTNRIGYHIPMFAGFVIMFLSTVMFAFSGTYTLLFVARTLQ  200
    |||||||||||||||||||||||.||:||||||.|||||||||||||||||
148 LLVNPFVGPLTNRIGYHIPMFVGFMIMFLSTLMFAFSGTYALLFVARTLQ  197

201 GIGSSFSSVAGLGMLASVYTDDHERGRAMGTALGGLALGLLVGAPFGSVM  250
    |||||||||||||||||||||.::|||||||.|||||||||||||||||||
198 GIGSSFSSVAGLGMLASVYTDNYERGRAMGIALGGLALGLLVGAPFGSVM  247
```

FIG.2A

251 YEFVGKSAPFLILAFLALLDGALQLCILQPSKVSPESAKGTPLFMLLKDP 300
        ||||||·|||||||||||||||||||||·||·|·||||··||||| ||||
248 YEFVGKSSPFLILAFLALLDGALQLCILWPSKVSPESAMGTSLLTLLKDP 297

301 YILVAAGSICFANMGVAILEPTLPIWMMQTMCSPKWQLGLAFLPASVSYL 350
        ||||||||||·|||||||||||||||||||||||·||||||||||||·||
298 YILVAAGSICLANMGVAILEPTLPIWMMQTMCSPEWQLGLAFLPASVAYL 347

351 IGTNLFGVLANKMGRWLCSLIGMLVVGTSLLCVPLAHKNFGLTGPNAGLG 400
        ||||||||||||||||||||·||·||·|·|||||||||·|·|||·||||||
348 IGTNLFGVLANKMGRWLCSLVGMVAVGISLLCVPLAHNIFGLIGPNAGLG 397

401 LXIGMVESSMMPIMGHLVDPRHTSVYGSVHAIADVAFCMGFAIGYSESGL 450
        ·||||·||·||||||·||||·||||||||·|||||||||·|||||·|·|·
398 FAIGMVDSSLMPIMGYLVDLRHTSVYGSVYAIADVAFCVGFAIGPSTGGV 447

451 PHGDPDVSTQKPLPWTSH 468
        ·|·· ··|·|·|
448 IVQVIGFPWLMVIIGTIN 465

FIG.2B